

Theme session B

Modernizing fisheries stock assessment with genetic methods for stock assessment and monitoring

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Introduction

Decision making for harvesting fish populations often relies on stock assessments that estimate population size but these estimates can be unreliable. Traditional stock assessments often use time-series data (index data and age structure analyses) that, through statistical procedures, can determine the stock's underlying production, reference points, as well as historical, current and projected biomass. Stock assessments can be prone to error when among other things, there are changes in the distribution of the stock relative to sampling frame of the abundance indices; lack of observations of the stock declining and rebuilding; unreliable catch data; lacking or unreliable age data and changes in stock's underlying production function due to climate change and ecological interactions. Further, for a variety of reasons, some commercial fish populations are not covered by current monitoring programmes. In addition, servicing the monitoring data needs for stock assessment can also be very expensive and moreover, to have ecosystem-scale assessment methods and modelling will further increase costs for monitoring and measurement by agencies. Given potential stock assessment errors and the costs of monitoring, examining and implementing alternatives to traditional stock assessment methods and monitoring are therefore highly relevant for fisheries management.

While population genetics tools have long been available for fisheries stock assessment and management, genetic/genomic methods have the potential to offer alternatives to traditional stock assessments and monitoring. For alternatives to traditional stock assessment, some new studies have used advanced genetic tools to estimate both exploitation rates, estimate absolute biomass for fish stocks, as well as population and individual fish identification, and also stock structure. These include: genetic mark-recapture for real-time harvest rate monitoring, absolute abundance of adult population size, mortality and age-specific relative reproductive output estimated by Close-Kin Mark-Recapture (CKMR), and parental-based tagging. For monitoring, Environmental DNA (eDNA) techniques promise new methods that can be used for monitoring communities and ecosystems. While there is much potential for genetic/genomic methods to improve stock assessment and monitoring, a number of questions need to be addressed in order to realize this potential.

The objective of the session was to address these questions, specifically:

- What genetic and associated statistical tools are available for resource monitoring and assessment?

- How can genetic methods for stock assessment and monitoring be applied to fisheries management in practice in order to provide more reliable tools to support integrated fisheries management advice? Inter alia: are genetic methods suitable to assess small/local populations, which may not be quantitatively assessed by traditional methods? What is the potential for eDNA to complement/replace current monitoring?
- Relative to existing techniques, under what circumstances do the genetic methods for stock assessment and monitoring offer more cost effective monitoring and stock assessment?
- What obstacles (practical, technological) need to be overcome in order to apply genetic methods for stock assessment and monitoring?

This report gives a brief overview of the session presentations and discussions. The contributions clearly addressed the objective of the session. Most contributions presented finished work, while some presented ongoing projects. The contributions could be split in three main themes: those dealing with CKMR, those dealing with gene flow and population structure, and those dealing with eDNA.

The CKMR contributions included reports about several finished studies. Speakers for these contributions included Mark Bravington and Hans Skaug, worldwide experts in the field. The finished studies were done on several tuna stocks (Southern bluefin tuna, Atlantic bluefin tuna) as well as on elasmobranchs (great white shark, spartooth shark). These studies suggest that CKMR is a powerful tool for estimating absolute abundance, survival rates, and other demographic parameters critical for management. The principle of it is that each offspring retrospectively "marks" its two parents; by comparing genotypes among a sample of fish, those marks can be "recaptured", either directly in the form of Parent-Offspring Pairs, or indirectly as Half-Sibling Pairs (one shared parent). The number of pairs found, and the associated covariates (age, year, etc.), can be embedded in a mark-recapture framework (structurally resembling an age-based stock assessment) to estimate demographic parameters of adults. In the case of the Atlantic bluefin tuna, sufficient genetic data could be collected from larval samples, and these data allowed identification of origin of parents from known stocks (West versus East Atlantic). Genetic differences among sampling locations are such that individual adults sampled from regions of mixed stock parentage can be assigned with close to 90% accuracy. In the example of the spartooth shark, half- and full-sibling pairs from single nucleotide polymorphism data and mitochondrial DNA informed whether sibling pairs were paternal or maternal. The model estimated abundance and spatial allocation of reproductive effort by sex across two rivers: Adelaide River, and Alligator River (Australia). High river fidelity was estimated for females and males in the Adelaide River. However, male sharks in the Alligator River were estimated to have a high chance of allocating reproductive output to the Adelaide River.

Within the North-East Atlantic, several CKMR projects have started in the last few years, and several projects contributed to the session by presenting status reports. These projects plan to contribute to the ICES advice by obtaining population abundance estimates for thornback ray in the Bay of Biscay and the North Sea and for white anglerfish in southern Celtic Seas and Bay of Biscay. None of these projects have finished yet, but the first results are expected to arrive soon. Practical issues met in these pioneering projects for collecting a large sample for stocks of moderate abundance such as thornback ray and for identifying informative genetic markers without a reference genome were shown. Although larger samples are required, sampling was shown to be probably easier and the cost to be proportionally smaller for more abundant species such as the white anglerfish, because the sample size required for a CKMR abundance estimation is proportional to the square root of the abundance.

With respect to the contributions on gene flow and population structure, the increased power of genomic tools to distinguish genotypes allow for new insights relevant for management. One example is the discovery of a spatial pattern in genotypes of the stock of turbot in the North Sea that points to one group of individuals being linked to the stratified region in the North of the North Sea and another group linked to the well-mixed region in the south. This spatial pattern can be related to the restriction in larval drift across the frontal zone between both waters in spring and summer. The existence of substructures in genetic populations is generally not dealt with in management of stocks. However, a possible framework for management of substocks was presented by Whitlock and coworkers. Their work included a spatially and seasonally-structured model of spawning migration for multiple salmon stocks. The model integrated genetic data (multilocus microsatellite genotypes) with prior information on abundance and movement for Baltic salmon. Spatio-temporal management actions for the mixed stock coastal fishery were then evaluated using Bayesian decision analysis.

The work on eDNA showed how this technique could be used for large scale biodiversity surveys. One example was a presentation on a Canadian initiative to sample 100 sites for eDNA. These samples were characterized at multiple taxonomic levels, ranging from marine viruses, bacteria, invertebrates, fishes, and mammals. Results for fishes and mammals were presented.

One of the challenges facing the eDNA field is to move beyond simple detection to quantitation. Several studies conducted eDNA sampling in parallel with trawl surveys. This allows a comparison of eDNA detections and relative abundances to traditional surveys. If eDNA can be successfully used for estimates of relative abundances then it can be used in classical stock assessments that require such relative trends in abundance. A study on Atlantic cod in Faroese waters by Salter and coworkers on eDNA using qPCR showed promising results, where local eDNA concentrations correlated with trawl survey estimates.

The conveners considered the session a success. The session clearly laid out the future potential for modern genetic methods to be used for stock assessment and monitoring. This was visible in the contributions to the sessions, the questions raised to speakers and the many discussions among the participants. Some had ample experience with these new techniques, others were curious researchers in the ICES community in the process of evaluating the opportunities that these new genetic techniques provide.